

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ARMITAGE, RICHARD
FANSLOW, WILLIAM
SPRIGGS, MELANIE
SRINIVASAN, SUBHASHINI
GIBSON, MARYLOU

(ii) TITLE OF INVENTION: NOVEL CYTOKINE

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: IMMUNEX CORPORATION
(B) STREET: 51 UNIVERSITY STREET
(C) CITY: SEATTLE
(D) STATE: WASHINGTON
(E) COUNTRY: USA
(F) ZIP: 98101

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: Apple Macintosh
(C) OPERATING SYSTEM: Apple Operating System 7.1
(D) SOFTWARE: Microsoft Word for Apple, version 5.1a

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/969,703
(B) FILING DATE: October 23, 1992
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/805,723
(B) FILING DATE: December 5, 1991
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/783,707
(B) FILING DATE: October 25, 1991
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Perkins, Patricia A.
(B) REGISTRATION NUMBER: 34,693
(C) REFERENCE/DOCKET NUMBER: 2802-C

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 2065870430
(B) TELEFAX: 2065870606

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 783 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: MOUSE

(vii) IMMEDIATE SOURCE:

15

(B) CLONE: CD40-L

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..783

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | |
|----|---|-----|
| 25 | ATG ATA GAA ACA TAC AGC CAA CCT TCC CCC AGA TCC GTG GCA ACT GGA | 48 |
| | Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly | |
| | 1 5 10 15 | |
| 30 | CTT CCA GCG AGC ATG AAG ATT TTT ATG TAT TTA CTT ACT GTT TTC CTT | 96 |
| | Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu | |
| | 20 25 30 | |
| 35 | ATC ACC CAA ATG ATT GGA TCT GTG CTT TTT GCT GTG TAT CTT CAT AGA | 144 |
| | Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg | |
| | 35 40 45 | |
| 40 | AGA TTG GAT AAG GTC GAA GAG GAA GTA AAC CTT CAT GAA GAT TTT GTA | 192 |
| | Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val | |
| | 50 55 60 | |
| 45 | TTC ATA AAA AAG CTA AAG AGA TGC AAC AAA GGA GAA GGA TCT TTA TCC | 240 |
| | Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser | |
| | 65 70 75 80 | |
| 50 | TTG CTG AAC TGT GAG GAG ATG AGA AGG CAA TTT GAA GAC CTT GTC AAG | 288 |
| | Leu Leu Asn Cys Glu Glu Met Arg Arg Phe Glu Asp Leu Val Lys | |
| | 85 90 95 | |
| 55 | GAT ATA ACG TTA AAC AAA GAA GAG AAA AAA GAA AAC AGC TTT GAA ATG | 336 |
| | Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met | |
| | 100 105 110 | |
| 60 | CAA AGA GGT GAT GAG GAT CCT CAA ATT GCA GCA CAC GTT GTA AGC GAA | 384 |
| | Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu | |
| | 115 120 125 | |
| 65 | GCC AAC AGT AAT GCA GCA TCC GTT CTA CAG TGG GCC AAG AAA GGA TAT | 432 |
| | Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr | |
| | 130 135 140 | |
| 70 | TAT ACC ATG AAA AGC AAC TTG GTA ATG CTT GAA AAT GGG AAA CAG CTG | 480 |
| | Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu | |
| | 145 150 155 160 | |

| | | |
|----|---|-----|
| | ACG GTT AAA AGA GAA GGA CTC TAT TAT GTC TAC ACT CAA GTC ACC TTC | 528 |
| | Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe | |
| | 165 170 175 | |
| 5 | TGC TCT AAT CGG GAG CCT TCG AGT CAA CGC CCA TTC ATC GTC GGC CTC | 576 |
| | Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu | |
| | 180 185 190 | |
| 10 | TGG CTG AAG CCC AGC AGT GGA TCT GAG AGA ATC TTA CTC AAG GCG GCA | 624 |
| | Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala | |
| | 195 200 205 | |
| 15 | AAT ACC CAC AGT TCC TCC CAG CTT TGC GAG CAG CAG TCT GTT CAC TTG | 672 |
| | Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu | |
| | 210 215 220 | |
| 20 | GGC GGA GTG TTT GAA TTA CAA GCT GGT GCT TCT GTG TTT GTC AAC GTG | 720 |
| | Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val | |
| | 225 230 235 240 | |
| 25 | ACT GAA GCA AGC CAA GTG ATC CAC AGA GTT GGC TTC TCA TCT TTT GGC | 768 |
| | Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly | |
| | 245 250 255 | |
| 30 | TTA CTC AAA CTC TGA | 783 |
| | Leu Leu Lys Leu | |
| | 260 | |
| 30 | (2) INFORMATION FOR SEQ ID NO:2: | |
| | (i) SEQUENCE CHARACTERISTICS: | |
| | (A) LENGTH: 260 amino acids | |
| | (B) TYPE: amino acid | |
| 35 | (D) TOPOLOGY: linear | |
| | (ii) MOLECULE TYPE: protein | |
| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: | |
| 40 | Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly | |
| | 1 5 10 15 | |
| 45 | Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu | |
| | 20 25 30 | |
| | Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg | |
| | 35 40 45 | |
| 50 | Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val | |
| | 50 55 60 | |
| 55 | Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser | |
| | 65 70 75 80 | |
| | Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys | |
| | 85 90 95 | |
| 60 | Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met | |
| | 100 105 110 | |
| | Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu | |
| | 115 120 125 | |

Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr
130 135 140

5 Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu
145 150 155 160

Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe
165 170 175

10 Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu
180 185 190

15 Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala
195 200 205

Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu
210 215 220

20 Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val
225 230 235 240

Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly
245 250 255

25 Leu Leu Lys Leu
260

30 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 740 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
45 (A) ORGANISM: HUMAN

(vii) IMMEDIATE SOURCE:
(B) CLONE: IgG1 Fc

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | |
|----|---|-----|
| | CGGTACCGCT AGCGTCGACA GGCCTAGGAT ATCGATACGT AGAGCCCAGA TCTGTGACA | 60 |
| 55 | AAACTCACAC ATGCCCACCG TGCCAGCAC CTGAACTCCT GGGGGGACCG TCAGTCTTCC | 120 |
| | TCTTCCCCC AAAACCCAAG GACACCCTCA TGATCTCCCG GACCCCTGAG GTCACATGCG | 180 |
| | TGGTGGTGGA CGTGAGCCAC GAAGACCCTG AGGTCAAGTT CAACTGGTAC GTGGACGGCG | 240 |
| 60 | TGGAGGTGCA TAATGCCAAG ACAAAGCCGC GGGAGGAGCA GTACAACAGC ACGTACCGGG | 300 |
| | TGGTCAGCGT CCTCACCGTC CTGCACCAGG ACTGGCTGAA TGGCAAGGAC TACAAGTGCA | 360 |

5 AGGTCTCCAA CAAAGCCCTC CCAGCCCCCA TGCAGAAAAC CATCTCCAAA GCCAAAGGGC 420
 AGCCCCGAGA ACCACAGGTG TACACCCTGC CCCCATCCCG GGATGAGCTG ACCAAGAACC 480
 AGGTCAGCCT GACCTGCCTG GTCAAAGGCT TCTATCCCAG GCACATCGCC GTGGAGTGGG 540
 AGAGCAATGG GCAGCCGGAG AACAACTACA AGACCACGCC TCCCGTGCTG GACTCCGACG 600
 10 GCTCCTTCTT CCTCTACAGC AAGCTCACCG TGGACAAGAG CAGGTGGCAG CAGGGGAACG 660
 TCTTCTCATG CTCCGTGATG CATGAGGCTC TGCACAACCA CTACACGCAG AAGAGCCTCT 720
 CCCTGTCTCC GGGTAAATGA 740

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HUMAN

(vii) IMMEDIATE SOURCE:

- (B) CLONE: CD40 EXTRACELLULAR REGION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

40 CAGAACACC CACTGCATGC AGAGAAAAAC AGTACCTAAT AAACAGTCAG TGCTGTTCTT 60
 TGTGCCAGCC AGGACAGAAA CTGGTGAGTG ACTGCACAGA GTTCACTGAA ACGGAATGCC 120
 TTCCTTGCGG TGAAAGCGAA TTCCTAGACA CCTGGAACAG AGAGACACAC TGCCACCAGC 180
 45 ACAAATACTG CGACCCCAAC CTAGGGCTTC GGTCCAGCA GAAGGGCACC TCAGAAACAG 240
 ACACCATCTG CACCTGTGAA GAAGGCTGGC ACTGTACGAG TGAGGCCTGT GAGAGCTGTG 300
 TCCTGCACCG CTCATGCTCG CCCGGCTTTG GGGTCAAGCA GATTGCTACA GGGGTTTCTG 360
 50 ATACCATCTG CGAGCCCTGC CCAGTCGGCT TCTTCTCCAA TGTGTCATCT GCTTTCGAAA 420
 AATGTCACCC TTGGACAAGC TGTGAGACCA AAGACCTGGT TGTGCAACAG GCAGGCACAA 480
 55 ACAAGACTGA TGTTGTCTGT GGTCCCCAGG ATCGGCTGA 519

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 10 (A) ORGANISM: PCR PRIMER
 (vii) IMMEDIATE SOURCE:
 (B) CLONE: CD40 5' PRIMER
 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
 CCGTCGACCA CCATGGTTCG TCTGCC
 20 (2) INFORMATION FOR SEQ ID NO:6:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 30 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PCR PRIMER
 35 (vii) IMMEDIATE SOURCE:
 (B) CLONE: CD40 3' PRIMER
 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
 CCGTCGACGT CTAGAGCCGA TCCTGGGG
 45 (2) INFORMATION FOR SEQ ID NO:7:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 (iii) HYPOTHETICAL: NO
 55 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: PCR PRIMER
 (vii) IMMEDIATE SOURCE:
 60 (B) CLONE: CD40 3' DOWNSTREAM PRIMER
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

26

28

ACAAGATCTG GGCTCTACGT ACTCAGCCGA TCCTGGGGAC

40

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PENTAPEPTIDE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Tyr Val Gly Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:
(B) CLONE: HUMAN IGG1/FC 5' PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TATTAATCAT TCAGTAGGGC CCAGATCTTG TGACAAAAC CAC

43

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:

(B) CLONE: HUMAN IGG1/FC 3' DOWNSTREAM PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCCAGCTTAA CTAGTTCATT TACCCGGAGA CAGGGAGA

38

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 840 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: CD40-L

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 46..831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCCACCTTC TCTGCCAGAA GATACCATTT CAACTTTAAC ACAGC ATG ATC GAA
Met Ile Glu

54

1

ACA TAC AAC CAA ACT TCT CCC CGA TCT GCG GCC ACT GGA CTG CCC ATC
Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly Leu Pro Ile
5 10 15

102

AGC ATG AAA ATT TTT ATG TAT TTA CTT ACT GTT TTT CTT ATC ACC CAG
Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu Ile Thr Gln
20 25 30 35

150

ATG ATT GGG TCA GCA CTT TTT GCT GTG TAT CTT CAT AGA AGG TTG GAC
Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg Arg Leu Asp
40 45 50

198

AAG ATA GAA GAT GAA AGG AAT CTT CAT GAA GAT TTT GTA TTC ATG AAA
Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys
55 60 65

246

ACG ATA CAG AGA TGC AAC ACA GGA GAA AGA TCC TTA TCC TTA CTG AAC
Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn
70 75 80

294

TGT GAG GAG ATT AAA AGC CAG TTT GAA GGC TTT GTG AAG GAT ATA ATG
Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met

342

85

90

95

5 TTA AAC AAA GAG GAG ACG AAG AAA GAA AAC AGC TTT GAA ATG CAA AAA 390
 Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys
 100 105 110 115
 GGT GAT CAG AAT CCT CAA ATT GCG GCA CAT GTC ATA AGT GAG GCC AGC 438
 Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser
 120 125 130
 10 AGT AAA ACA ACA TCT GTG TTA CAG TGG GCT GAA AAA GGA TAC TAC ACC 486
 Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr
 135 140 145
 15 ATG AGC AAC AAC TTG GTA ACC CTG GAA AAT GGG AAA CAG CTG ACC GTT 534
 Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val
 150 155 160
 20 AAA AGA CAA GGA CTC TAT TAT ATC TAT GCC CAA GTC ACC TTC TGT TCC 582
 Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser
 165 170 175
 AAT CGG GAA GCT TCG AGT CAA GCT CCA TTT ATA GCC AGC CTC TGC CTA 630
 Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu
 180 185 190 195
 AAG TCC CCC GGT AGA TTC GAG AGA ATC TTA CTC AGA GCT GCA AAT ACC 678
 Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr
 200 205 210
 30 CAC AGT TCC GCC AAA CCT TGC GGG CAA CAA TCC ATT CAC TTG GGA GGA 726
 His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly
 215 220 225
 35 GTA TTT GAA TTG CAA CCA GGT GCT TCG GTG TTT GTC AAT GTG ACT GAT 774
 Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp
 230 235 240
 40 CCA AGC CAA GTG AGC CAT GGC ACT GGC TTC ACG TCC TTT GGC TTA CTC 822
 Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu
 245 250 255
 AAA CTC TGAACAGTGT CA 840
 Lys Leu
 45 260

(2) INFORMATION FOR SEQ ID NO:12:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

60 Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly
 1 5 10 15
 Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
 20 25 30

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Ile | Thr | Gln | Met | Ile | Gly | Ser | Ala | Leu | Phe | Ala | Val | Tyr | Leu | His | Arg | |
| | | | 35 | | | | | 40 | | | | | 45 | | | | |
| 5 | Arg | Leu | Asp | Lys | Ile | Glu | Asp | Glu | Arg | Asn | Leu | His | Glu | Asp | Phe | Val | |
| | | 50 | | | | | 55 | | | | | 60 | | | | | |
| | Phe | Met | Lys | Thr | Ile | Gln | Arg | Cys | Asn | Thr | Gly | Glu | Arg | Ser | Leu | Ser | |
| | 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| 10 | Leu | Leu | Asn | Cys | Glu | Glu | Ile | Lys | Ser | Gln | Phe | Glu | Gly | Phe | Val | Lys | |
| | | | | | 85 | | | | | 90 | | | | | 95 | | |
| | Asp | Ile | Met | Leu | Asn | Lys | Glu | Glu | Thr | Lys | Lys | Glu | Asn | Ser | Phe | Glu | |
| 15 | | | | 100 | | | | | 105 | | | | | 110 | | | |
| | Met | Gln | Lys | Gly | Asp | Gln | Asn | Pro | Gln | Ile | Ala | Ala | His | Val | Ile | Ser | |
| | | | 115 | | | | | 120 | | | | | 125 | | | | |
| 20 | Glu | Ala | Ser | Ser | Lys | Thr | Thr | Ser | Val | Leu | Gln | Trp | Ala | Glu | Lys | Gly | |
| | | 130 | | | | | 135 | | | | | 140 | | | | | |
| | Tyr | Tyr | Thr | Met | Ser | Asn | Asn | Leu | Val | Thr | Leu | Glu | Asn | Gly | Lys | Gln | |
| | 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| 25 | Leu | Thr | Val | Lys | Arg | Gln | Gly | Leu | Tyr | Tyr | Ile | Tyr | Ala | Gln | Val | Thr | |
| | | | | 165 | | | | | 170 | | | | | | 175 | | |
| | Phe | Cys | Ser | Asn | Arg | Glu | Ala | Ser | Ser | Gln | Ala | Pro | Phe | Ile | Ala | Ser | |
| 30 | | | | 180 | | | | | 185 | | | | | 190 | | | |
| | Leu | Cys | Leu | Lys | Ser | Pro | Gly | Arg | Phe | Glu | Arg | Ile | Leu | Leu | Arg | Ala | |
| | | | 195 | | | | | 200 | | | | | 205 | | | | |
| 35 | Ala | Asn | Thr | His | Ser | Ser | Ala | Lys | Pro | Cys | Gly | Gln | Gln | Ser | Ile | His | |
| | | 210 | | | | | 215 | | | | | 220 | | | | | |
| | Leu | Gly | Gly | Val | Phe | Glu | Leu | Gln | Pro | Gly | Ala | Ser | Val | Phe | Val | Asn | |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| 40 | Val | Thr | Asp | Pro | Ser | Gln | Val | Ser | His | Gly | Thr | Gly | Phe | Thr | Ser | Phe | |
| | | | | | 245 | | | | | 250 | | | | | 255 | | |
| | Gly | Leu | Leu | Lys | Leu | | | | | | | | | | | | |
| 45 | | | | 260 | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:13:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- 60 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGGTGGCGGA GGGTCAGGCG GAGGTGGGTC CGGAGGCGGG GGTCAAGTT CTGACAAGAT 60
5 AGAAGATGAA AGG 73

(2) INFORMATION FOR SEQ ID NO:14:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

20 (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

25 GGCCGCTCAG AGTTTGAGTA A 21

(2) INFORMATION FOR SEQ ID NO:15:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

40 (iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: Human CD40-L/FC2 (soluble CD40-L)

45 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 4..1422

50 (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 79..1422

55 (ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 4..78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

60 TAT ATG TTC CAT GTT TCT TTT AGA TAT ATC TTT GGA ATT CCT CCA CTG 48
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu
-25 -20 -15

| | | |
|----|---|-----|
| | ATC CTT GTT CTG CTG CCT GTC ACT AGC TCT GAC TAC AAA GAT GAC GAT Ile Leu Val Leu Leu Pro Val Thr Ser Ser Asp Tyr Lys Asp Asp Asp -10 -5 1 5 | 96 |
| 5 | GAT AAA AGA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA Asp Lys Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala 10 15 20 | 144 |
| 10 | CCT GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro 25 30 35 | 192 |
| 15 | AAG GAC ACC CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val 40 45 50 | 240 |
| 20 | GTG GAC GTG AGC CAC GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val 55 60 65 70 | 288 |
| 25 | GAC GGC GTG GAG GTG CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln 75 80 85 | 336 |
| 30 | TAC AAC AGC ACG TAC CGG GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln 90 95 100 | 384 |
| 35 | GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala 105 110 115 | 432 |
| 40 | CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro 120 125 130 | 480 |
| 45 | CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG ACC Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr 135 140 145 150 | 528 |
| 50 | AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser 155 160 165 | 576 |
| 55 | GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr 170 175 180 | 624 |
| 60 | AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr 185 190 195 | 672 |
| 65 | AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe 200 205 210 | 720 |
| 70 | TCA TGC TCC GTG ATG CAT GGT GGC GGA GGG TCA GGC GGA GGT GGG TCC Ser Cys Ser Val Met His Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser 215 220 225 230 | 768 |
| 75 | GGA GGC GGG GGT TCA AGT TCT GAC AAG ATA GAA GAT GAA AGG AAT CTT Gly Gly Gly Gly Ser Ser Ser Asp Lys Ile Glu Asp Glu Arg Asn Leu 235 240 245 | 816 |

| | | |
|----|---|------|
| | CAT GAA GAT TTT GTA TTC ATG AAA ACG ATA CAG AGA TGC AAC ACA GGA | 864 |
| | His Glu Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly | |
| | 250 255 260 | |
| 5 | GAA AGA TCC TTA TCC TTA CTG AAC TGT GAG GAG ATT AAA AGC CAG TTT | 912 |
| | Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe | |
| | 265 270 275 | |
| 10 | GAA GGC TTT GTG AAG GAT ATA ATG TTA AAC AAA GAG GAG ACG AAG AAA | 960 |
| | Glu Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys | |
| | 280 285 290 | |
| 15 | GAA AAC AGC TTT GAA ATG CAA AAA GGT GAT CAG AAT CCT CAA ATT GCG | 1008 |
| | Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala | |
| | 295 300 305 310 | |
| 20 | GCA CAT GTC ATA AGT GAG GCC AGC AGT AAA ACA ACA TCT GTG TTA CAG | 1056 |
| | Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln | |
| | 315 320 325 | |
| | TGG GCT GAA AAA GGA TAC TAC ACC ATG AGC AAC AAC TTG GTA ACC CTG | 1104 |
| | Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu | |
| | 330 335 340 | |
| 25 | GAA AAT GGG AAA CAG CTG ACC GTT AAA AGA CAA GGA CTC TAT TAT ATC | 1152 |
| | Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile | |
| | 345 350 355 | |
| 30 | TAT GCC CAA GTC ACC TTC TGT TCC AAT CGG GAA GCT TCG AGT CAA GCT | 1200 |
| | Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala | |
| | 360 365 370 | |
| 35 | CCA TTT ATA GCC AGC CTC TGC CTA AAG TCC CCC GGT AGA TTC GAG AGA | 1248 |
| | Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg | |
| | 375 380 385 390 | |
| 40 | ATC TTA CTC AGA GCT GCA AAT ACC CAC AGT TCC GCC AAA CCT TGC GGG | 1296 |
| | Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly | |
| | 395 400 405 | |
| | CAA CAA TCC ATT CAC TTG GGA GGA GTA TTT GAA TTG CAA CCA GGT GCT | 1344 |
| | Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala | |
| | 410 415 420 | |
| 45 | TCG GTG TTT GTC AAT GTG ACT GAT CCA AGC CAA GTG AGC CAT GGC ACT | 1392 |
| | Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr | |
| | 425 430 435 | |
| 50 | GGC TTC ACG TCC TTT GGC TTA CTC AAA CTC TGA | 1425 |
| | Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu | |
| | 440 445 | |

55 (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 473 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
-25 -20 -15 -10

5 Leu Val Leu Leu Pro Val Thr Ser Ser Asp Tyr Lys Asp Asp Asp Asp
-5 1 5

10 Lys Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
10 15 20

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
25 30 35

15 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
40 45 50 55

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
60 65 70

20 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
75 80 85

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
90 95 100

25 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
105 110 115

30 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
120 125 130 135

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
140 145 150

35 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
155 160 165

40 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
170 175 180

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
185 190 195

45 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
200 205 210 215

Cys Ser Val Met His Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
220 225 230

50 Gly Gly Gly Ser Ser Ser Asp Lys Ile Glu Asp Glu Arg Asn Leu His
235 240 245

55 Glu Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu
250 255 260

Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu
265 270 275

60 Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu
280 285 290 295

Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala

300

305

310

His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp
 315 320 325

5 Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu
 330 335 340

10 Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr
 345 350 355

Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro
 360 365 370 375

15 Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile
 380 385 390

Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln
 395 400 405

20 Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser
 410 415 420

25 Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly
 425 430 435

Phe Thr Ser Phe Gly Leu Leu Lys Leu
 440 445

30 (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile
 1 5 10 15

45 Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu
 20 25 30

Arg

50

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: DNA

60

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATATGAATTC GACTACAAAG ATGACGATGA TAAACCTCAA ATTGCAGCAC ACGTT

21

(2) INFORMATION FOR SEQ ID NO:19:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTTCGCGGC CGCGTTCAGA GTTTGAGTAA GCCAA

35

(2) INFORMATION FOR SEQ ID NO:20:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 929 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

40 (A) ORGANISM: Human CD40-L trimer

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 65..142

45 (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 65..886

50 (ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 143..886

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGAGCGAGTC CGCATCGACG GATCGGAAAA CCTCTCCGAG GTACCTATCC CGGGGATCCC

60

60 CACC ATG TTC CAT GTT TCT TTT AGA TAT ATC TTT GGA ATT CCT CCA CTG
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu
-26 -25 -20 -15

109

ATC CTT GTT CTG CTG CCT GTC ACT AGT TCT GAC CGT ATG AAA CAG ATA

157

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | Ile | Leu | Val | Leu | Leu | Pro | Val | Thr | Ser | Ser | Asp | Arg | Met | Lys | Gln | Ile | |
| | -10 | | | | | | -5 | | | | | 1 | | | | 5 | |
| 5 | GAG | GAT | AAG | ATC | GAA | GAG | ATC | CTA | AGT | AAG | ATT | TAT | CAT | ATA | GAG | AAT | 205 |
| | Glu | Asp | Lys | Ile | Glu | Glu | Ile | Leu | Ser | Lys | Ile | Tyr | His | Ile | Glu | Asn | |
| | | | | | 10 | | | | | 15 | | | | | 20 | | |
| 10 | GAA | ATC | GCC | CGT | ATC | AAA | AAG | CTG | ATT | GGC | GAG | CGG | ACT | AGT | TCT | GAC | 253 |
| | Glu | Ile | Ala | Arg | Ile | Lys | Lys | Leu | Ile | Gly | Glu | Arg | Thr | Ser | Ser | Asp | |
| | | | | 25 | | | | 30 | | | | | 35 | | | | |
| 15 | AAG | ATA | GAA | GAT | GAA | AGG | AAT | CTT | CAT | GAA | GAT | TTT | GTA | TTC | ATG | AAA | 301 |
| | Lys | Ile | Glu | Asp | Glu | Arg | Asn | Leu | His | Glu | Asp | Phe | Val | Phe | Met | Lys | |
| | | | 40 | | | | 45 | | | | | | 50 | | | | |
| 20 | ACG | ATA | CAG | AGA | TGC | AAC | ACA | GGA | GAA | AGA | TCC | TTA | TCC | TTA | CTG | AAC | 349 |
| | Thr | Ile | Gln | Arg | Cys | Asn | Thr | Gly | Glu | Arg | Ser | Leu | Ser | Leu | Leu | Asn | |
| | | 55 | | | | | 60 | | | | | 65 | | | | | |
| 25 | TGT | GAG | GAG | ATT | AAA | AGC | CAG | TTT | GAA | GGC | TTT | GTG | AAG | GAT | ATA | ATG | 397 |
| | Cys | Glu | Glu | Ile | Lys | Ser | Gln | Phe | Glu | Gly | Phe | Val | Lys | Asp | Ile | Met | |
| | | 70 | | | | 75 | | | | | 80 | | | | | 85 | |
| 30 | TTA | AAC | AAA | GAG | GAG | ACG | AAG | AAA | GAA | AAC | AGC | TTT | GAA | ATG | CAA | AAA | 445 |
| | Leu | Asn | Lys | Glu | Glu | Thr | Lys | Lys | Glu | Asn | Ser | Phe | Glu | Met | Gln | Lys | |
| | | | | | 90 | | | | | 95 | | | | | 100 | | |
| 35 | GGT | GAT | CAG | AAT | CCT | CAA | ATT | GCG | GCA | CAT | GTC | ATA | AGT | GAG | GCC | AGC | 493 |
| | Gly | Asp | Gln | Asn | Pro | Gln | Ile | Ala | Ala | His | Val | Ile | Ser | Glu | Ala | Ser | |
| | | | | 105 | | | | 110 | | | | | | 115 | | | |
| 40 | AGT | AAA | ACA | ACA | TCT | GTG | TTA | CAG | TGG | GCT | GAA | AAA | GGA | TAC | TAC | ACC | 541 |
| | Ser | Lys | Thr | Thr | Ser | Val | Leu | Gln | Trp | Ala | Glu | Lys | Gly | Tyr | Tyr | Thr | |
| | | | 120 | | | | 125 | | | | | | 130 | | | | |
| 45 | ATG | AGC | AAC | AAC | TTG | GTA | ACC | CTG | GAA | AAT | GGG | AAA | CAG | CTG | ACC | GTT | 589 |
| | Met | Ser | Asn | Asn | Leu | Val | Thr | Leu | Glu | Asn | Gly | Lys | Gln | Leu | Thr | Val | |
| | | 135 | | | | | 140 | | | | | 145 | | | | | |
| 50 | AAA | AGA | CAA | GGA | CTC | TAT | TAT | ATC | TAT | GCC | CAA | GTC | ACC | TTC | TGT | TCC | 637 |
| | Lys | Arg | Gln | Gly | Leu | Tyr | Tyr | Ile | Tyr | Ala | Gln | Val | Thr | Phe | Cys | Ser | |
| | | 150 | | | | 155 | | | | | 160 | | | | | 165 | |
| 55 | AAT | CGG | GAA | GCT | TCG | AGT | CAA | GCT | CCA | TTT | ATA | GCC | AGC | CTC | TGC | CTA | 685 |
| | Asn | Arg | Glu | Ala | Ser | Ser | Gln | Ala | Pro | Phe | Ile | Ala | Ser | Leu | Cys | Leu | |
| | | | | 170 | | | | | | 175 | | | | | 180 | | |
| 60 | AAG | TCC | CCC | GGT | AGA | TTC | GAG | AGA | ATC | TTA | CTC | AGA | GCT | GCA | AAT | ACC | 733 |
| | Lys | Ser | Pro | Gly | Arg | Phe | Glu | Arg | Ile | Leu | Leu | Arg | Ala | Ala | Asn | Thr | |
| | | | | 185 | | | | | 190 | | | | | 195 | | | |
| 65 | CAC | AGT | TCC | GCC | AAA | CCT | TGC | GGG | CAA | CAA | TCC | ATT | CAC | TTG | GGA | GGA | 781 |
| | His | Ser | Ser | Ala | Lys | Pro | Cys | Gly | Gln | Gln | Ser | Ile | His | Leu | Gly | Gly | |
| | | | 200 | | | | 205 | | | | | | 210 | | | | |
| 70 | GTA | TTT | GAA | TTG | CAA | CCA | GGT | GCT | TCG | GTG | TTT | GTC | AAT | GTG | ACT | GAT | 829 |
| | Val | Phe | Glu | Leu | Gln | Pro | Gly | Ala | Ser | Val | Phe | Val | Asn | Val | Thr | Asp | |
| | | 215 | | | | | 220 | | | | | 225 | | | | | |
| 75 | CCA | AGC | CAA | GTG | AGC | CAT | GGC | ACT | GGC | TTC | ACG | TCC | TTT | GGC | TTA | CTC | 877 |
| | Pro | Ser | Gln | Val | Ser | His | Gly | Thr | Gly | Phe | Thr | Ser | Phe | Gly | Leu | Leu | |
| | | 230 | | | | 235 | | | | | 240 | | | | | 245 | |

5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
-26 -25 -20 -15
Leu Val Leu Leu Pro Val Thr Ser Ser Asp Arg Met Lys Gln Ile Glu
-10 -5 1 5
Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu
10 15 20
Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Ser Ser Asp Lys
25 25 30 35
Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr
30 40 45 50
Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys
55 60 65 70
Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu
75 80 85
Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly
90 95 100
Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser
105 110 115
Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met
120 125 130
Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys
135 140 145 150
Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn
155 160 165
Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys
170 175 180
Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His
185 190 195
Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val
200 205 210
Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro
215 220 225 230

Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys
235 240 245

5 Leu

(2) INFORMATION FOR SEQ ID NO:22:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 878 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
(B) CLONE: Murine CD40-L trimer

20 (ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION: 15..92

25 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 15..857

30 (ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 93..857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

35 CTCGAGGTAC CGCC ATG TTC CAT GTT TCT TTT AGA TAT ATC TTT GGA ATT 50
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile
-26 -25 -20 -15

40 CCT CCA CTG ATC CTT GTT CTG CTG CCT GTC ACT AGT TCT GAC CGT ATG 98
Pro Pro Leu Ile Leu Val Leu Leu Pro Val Thr Ser Ser Asp Arg Met
-10 -5 1

45 AAA CAG ATA GAG GAT AAG ATC GAA GAG ATC CTA AGT AAG ATT TAT CAT 146
Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His
5 10 15

50 ATA GAG AAT GAA ATC GCC CGT ATC AAA AAG CTG ATT GGC GAG CGG ACT 194
Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr
20 25 30

AGT TCT GAC TAC AAA GAT GAC GAT GAT AAA GAT AAG GTC GAA GAG GAA 242
Ser Ser Asp Tyr Lys Asp Asp Asp Asp Lys Asp Lys Val Glu Glu Glu
35 40 45 50

55 GTA AAC CTT CAT GAA GAT TTT GTA TTC ATA AAA AAG CTA AAG AGA TGC 290
Val Asn Leu His Glu Asp Phe Val Phe Ile Lys Lys Leu Lys Arg Cys
55 60 65

60 AAC AAA GGA GAA GGA TCT TTA TCC TTG CTG AAC TGT GAG GAG ATG AGA 338
Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys Glu Glu Met Arg
70 75 80

| | | |
|----|---|-----|
| | AGG CAA TTT GAA GAC CTT GTC AAG GAT ATA ACG TTA AAC AAA GAA GAG | 386 |
| | Arg Gln Phe Glu Asp Leu Val Lys Asp Ile Thr Leu Asn Lys Glu Glu | |
| | 85 90 95 | |
| 5 | AAA AAA GAA AAC AGC TTT GAA ATG CAA AGA GGT GAT GAG GAT CCT CAA | 434 |
| | Lys Lys Glu Asn Ser Phe Glu Met Gln Arg Gly Asp Glu Asp Pro Gln | |
| | 100 105 110 | |
| 10 | ATT GCA GCA CAC GTT GTA AGC GAA GCC AAC AGT AAT GCA GCA TCC GTT | 482 |
| | Ile Ala Ala His Val Val Ser Glu Ala Asn Ser Asn Ala Ala Ser Val | |
| | 115 120 125 130 | |
| 15 | CTA CAG TGG GCC AAG AAA GGA TAT TAT ACC ATG AAA AGC AAC TTG GTA | 530 |
| | Leu Gln Trp Ala Lys Lys Gly Tyr Tyr Thr Met Lys Ser Asn Leu Val | |
| | 135 140 145 | |
| 20 | ATG CTT GAA AAT GGG AAA CAG CTG ACG GTT AAA AGA GAA GGA CTC TAT | 578 |
| | Met Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Glu Gly Leu Tyr | |
| | 150 155 160 | |
| 25 | TAT GTC TAC ACT CAA GTC ACC TTC TGC TCT AAT CGG GAG CCT TCG AGT | 626 |
| | Tyr Val Tyr Thr Gln Val Thr Phe Cys Ser Asn Arg Glu Pro Ser Ser | |
| | 165 170 175 | |
| 30 | CAA CGC CCA TTC ATC GTC GGC CTC TGG CTG AAG CCC AGC AGT GGA TCT | 674 |
| | Gln Arg Pro Phe Ile Val Gly Leu Trp Leu Lys Pro Ser Ser Gly Ser | |
| | 180 185 190 | |
| 35 | GAG AGA ATC TTA CTC AAG GCG GCA AAT ACC CAC AGT TCC TCC CAG CTT | 722 |
| | Glu Arg Ile Leu Leu Lys Ala Ala Asn Thr His Ser Ser Ser Gln Leu | |
| | 195 200 205 210 | |
| 40 | TGC GAG CAG CAG TCT GTT CAC TTG GGC GGA GTG TTT GAA TTA CAA GCT | 770 |
| | Cys Glu Gln Gln Ser Val His Leu Gly Gly Val Phe Glu Leu Gln Ala | |
| | 215 220 225 | |
| 45 | GGT GCT TCT GTG TTT GTC AAC GTG ACT GAA GCA AGC CAA GTG ATC CAC | 818 |
| | Gly Ala Ser Val Phe Val Asn Val Thr Glu Ala Ser Gln Val Ile His | |
| | 230 235 240 | |
| 50 | AGA GTT GGC TTC TCA TCT TTT GGC TTA CTC AAA CTC TGAACGCGGC | 864 |
| | Arg Val Gly Phe Ser Ser Phe Gly Leu Leu Lys Leu | |
| | 245 250 255 | |
| 55 | CGCTACAGAT CTAC | 878 |

(2) INFORMATION FOR SEQ ID NO:23:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 280 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

60 Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
 -26 -25 -20 -15
 Leu Val Leu Leu Pro Val Thr Ser Ser Asp Arg Met Lys Gln Ile Glu
 -10 -5 1 5

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | Asp | Lys | Ile | Glu | Glu | Ile | Leu | Ser | Lys | Ile | Tyr | His | Ile | Glu | Asn | Glu | |
| | | | | 10 | | | | | 15 | | | | | 20 | | | |
| 5 | Ile | Ala | Arg | Ile | Lys | Lys | Leu | Ile | Gly | Glu | Arg | Thr | Ser | Ser | Asp | Tyr | |
| | | | 25 | | | | | 30 | | | | | 35 | | | | |
| | Lys | Asp | Asp | Asp | Asp | Lys | Asp | Lys | Val | Glu | Glu | Glu | Val | Asn | Leu | His | |
| | | 40 | | | | | 45 | | | | | 50 | | | | | |
| 10 | Glu | Asp | Phe | Val | Phe | Ile | Lys | Lys | Leu | Lys | Arg | Cys | Asn | Lys | Gly | Glu | |
| | | 55 | | | | 60 | | | | | 65 | | | | | 70 | |
| | Gly | Ser | Leu | Ser | Leu | Leu | Asn | Cys | Glu | Glu | Met | Arg | Arg | Gln | Phe | Glu | |
| 15 | | | | | 75 | | | | | 80 | | | | | 85 | | |
| | Asp | Leu | Val | Lys | Asp | Ile | Thr | Leu | Asn | Lys | Glu | Glu | Lys | Lys | Glu | Asn | |
| | | | | 90 | | | | | 95 | | | | | 100 | | | |
| 20 | Ser | Phe | Glu | Met | Gln | Arg | Gly | Asp | Glu | Asp | Pro | Gln | Ile | Ala | Ala | His | |
| | | | 105 | | | | | 110 | | | | | 115 | | | | |
| | Val | Val | Ser | Glu | Ala | Asn | Ser | Asn | Ala | Ala | Ser | Val | Leu | Gln | Trp | Ala | |
| | | | 120 | | | | 125 | | | | | 130 | | | | | |
| 25 | Lys | Lys | Gly | Tyr | Tyr | Thr | Met | Lys | Ser | Asn | Leu | Val | Met | Leu | Glu | Asn | |
| | | 135 | | | | 140 | | | | | 145 | | | | | 150 | |
| | Gly | Lys | Gln | Leu | Thr | Val | Lys | Arg | Glu | Gly | Leu | Tyr | Tyr | Val | Tyr | Thr | |
| 30 | | | | | 155 | | | | | 160 | | | | | 165 | | |
| | Gln | Val | Thr | Phe | Cys | Ser | Asn | Arg | Glu | Pro | Ser | Ser | Gln | Arg | Pro | Phe | |
| | | | | 170 | | | | | 175 | | | | | 180 | | | |
| 35 | Ile | Val | Gly | Leu | Trp | Leu | Lys | Pro | Ser | Ser | Gly | Ser | Glu | Arg | Ile | Leu | |
| | | | 185 | | | | | 190 | | | | | 195 | | | | |
| | Leu | Lys | Ala | Ala | Asn | Thr | His | Ser | Ser | Ser | Gln | Leu | Cys | Glu | Gln | Gln | |
| | | 200 | | | | | 205 | | | | | 210 | | | | | |
| 40 | Ser | Val | His | Leu | Gly | Gly | Val | Phe | Glu | Leu | Gln | Ala | Gly | Ala | Ser | Val | |
| | | 215 | | | | 220 | | | | | 225 | | | | | 230 | |
| | Phe | Val | Asn | Val | Thr | Glu | Ala | Ser | Gln | Val | Ile | His | Arg | Val | Gly | Phe | |
| 45 | | | | | 235 | | | | | 240 | | | | | 245 | | |
| | Ser | Ser | Phe | Gly | Leu | Leu | Lys | Leu | | | | | | | | | |
| | | | | 250 | | | | | | | | | | | | | |